

SEQUENCE LISTING

# 9/18/95

(1) GENERAL INFORMATION:

- (i) APPLICANT: HU, JING-SHAN  
OLSEN, HENRIK  
ROSEN, CRAIG G.
- (ii) TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING VASCULAR  
ENDOTHELIAL GROWTH FACTOR 3 POLYPEPTIDES AND METHODS FOR  
PRODUCING THE POLYPEPTIDES

(iii) NUMBER OF SEQUENCES: 8

- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
  - (B) STREET: 1100 NEW YORK AVE, NW
  - (C) CITY: WASHINGTON
  - (D) STATE: DC
  - (E) COUNTRY: USA
  - (F) ZIP: 20005

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/469,641
- (B) FILING DATE: 06-JUN-1995
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: STEFFE, ERIC K.
- (B) REGISTRATION NUMBER: 36,688
- (C) REFERENCE/DOCKET NUMBER: 1488.1040000

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-371-2600
- (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 666 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG AGA AGG TGT AGA ATA AGT GGG AGG CCC CCG GCG CCC CCC GGT GTC Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly Val 1 5 10 15	48
CCC GCC CAG GCC CCT GTC TCC CAG CCT GAT GCC CCT GGC CAC CAG AGG Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln Arg 20 25 30	96
AAA GTG GTG TCA TGG ATA GAT GTG TAT ACT CGC GCT ACC TGC CAG CCC Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln Pro 35 40 45	144
CGG GAG GTG GTG GTG CCC TTG ACT GTG GAG CTC ATG GGC ACC GTG GCC Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val Ala 50 55 60	192
AAA CAG CTG GTG CCC AGC TGC GTG ACT GTG CAG CGC TGT GGT GGC TGC Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys 65 70 75 80	240
TGC CCT GAC GAT GGC CTG GAG TGT GTG CCC ACT GGG CAG CAC CAA GTC Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val 85 90 95	288
CGG ATG CAG ATC CTC ATG ATC CGG TAC CCG AGC AGT CAG CTG GGG GAG Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly Glu 100 105 110	336
ATG TCC CTG GAA GAA CAC AGC CAG TGT GAA TGC AGA CCT AAA AAA AAG Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys 115 120 125	384
GAC AGT GCT GTG AAG CCA GAC AGG GCT GCT ACT CCC CAC CAC CGT CCC Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro 130 135 140	432
CAG CCC CGT TCT GTT CCG GGC TGG GAC TCT GCC CCC GGA GCA CCC TCC Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser 145 150 155 160	480
CCA GCT GAC ATC ACC CAA TCC CAC TCC AGC CCC AGG CCC CTC TGC CCA Pro Ala Asp Ile Thr Gln Ser His Ser Ser Pro Arg Pro Leu Cys Pro 165 170 175	528
CGC TGC ACC CAG CAC CAC CAG TGC CCT GAC CCC CGG ACC TGC CGC TGC Arg Cys Thr Gln His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys 180 185 190	576
CGC TGT CGA CGC CGC AGC TTC CTC CGT TGT CAA GGG CGG GGC TTA GAG Arg Cys Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu 195 200 205	624
CTC AAC CCA GAC ACC TGC AGG TGC CGG AAG CTG CGA AGG TGA Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg 210 215 220	666

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 221 amino acids
  - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Arg Cys Arg Ile Ser Gly Arg Pro Pro Ala Pro Pro Gly Val  
1 5 10 15

Pro Ala Gln Ala Pro Val Ser Gln Pro Asp Ala Pro Gly His Gln Arg  
20 25 30

Lys Val Val Ser Trp Ile Asp Val Tyr Thr Arg Ala Thr Cys Gln Pro  
35 40 45

Arg Glu Val Val Val Pro Leu Thr Val Glu Leu Met Gly Thr Val Ala  
50 55 60

Lys Gln Leu Val Pro Ser Cys Val Thr Val Gln Arg Cys Gly Gly Cys  
65 70 75 80

Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln His Gln Val  
85 90 95

Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln Leu Gly Glu  
100 105 110

Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys Arg Pro Lys Lys Lys  
115 120 125

Asp Ser Ala Val Lys Pro Asp Arg Ala Ala Thr Pro His His Arg Pro  
130 135 140

Gln Pro Arg Ser Val Pro Gly Trp Asp Ser Ala Pro Gly Ala Pro Ser  
145 150 155 160

Pro Ala Asp Ile Thr Gln Ser His Ser Pro Arg Pro Leu Cys Pro  
165 170 175

Arg Cys Thr Gln His His Gln Cys Pro Asp Pro Arg Thr Cys Arg Cys  
180 185 190

Arg Cys Arg Arg Arg Ser Phe Leu Arg Cys Gln Gly Arg Gly Leu Glu  
195 200 205

Leu Asn Pro Asp Thr Cys Arg Cys Arg Lys Leu Arg Arg  
210 215 220

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCATGGATCC CAGCCTGATG CCCCTGGCC

29

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCATTCTAGA CCCTGCTGAG TCTGAAAAGC

30

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACTGCATGC ACCAGAGGAA AGTGGTGTC

29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GACTAGATCT CCTTCGCAGC TTCCGGCAC

29

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Xaa Cys Val Xaa Xaa Xaa Arg Cys Xaa Gly Cys Cys Cys Asn  
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val  
130 135 140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Ser Arg Tyr  
145 150 155 160

Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His  
165 170 175

Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr  
180 185 190

Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys

195

200

205

Arg Cys Asp Lys Pro Arg Arg  
210 215